

FASTA searches a protein or DNA sequence data bank  
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaCAAyBaGwh: 3571 aa  
>gi|40198414|gb|AAR79125.1| Sequence 2 from patent US 6656707  
vs /tmp/fastaDAAzBaGwh library  
searching /tmp/fastaDAAzBaGwh library

3571 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2

join: 47, opt: 35, gap-pen: -12/ -2, width: 16

Scan time: 0.117

The best scores are:

opt

SEQ ID NO:4

(3571) 25785

>>SEQ ID NO:4

(3571 aa)

initn: 25785 initl: 25785 opt: 25785

Smith-Waterman score: 25785; 99.860% identity in 3571 aa overlap (1-3571:1-3571)

	10	20	30	40	50	60
gi 401	MWPRLAFCCWGLALVSGWATFQQMSPSRNFSFRLFPETAPGAPGSIPAPPAPGDEAAGSR					
	10	20	30	40	50	60
SEQ	MWPRLAFCCWGLALVSGWATFQQMSPSRNFSFRLFPETAPGAPGSIPAPPAPGDEAAGSR					
	70	80	90	100	110	120
gi 401	VERLGQAFRRRVRLRELSELELVFLVDDSSSVGEVNFRLSELMFVRKLLSDFPVVPTAT					
	70	80	90	100	110	120
SEQ	VERLGQAFRRRVRLRELSELELVFLVDDSSSVGEVNFRLSELMFVRKLLSDFPVVPTAT					
	130	140	150	160	170	180
gi 401	RVAIVTFSSKNYVVPVVDYISTRARQHKALLLQEIPAISSYRGGGTYTKGAFQQAQIL					
	130	140	150	160	170	180
SEQ	RVAIVTFSSKNYVVPVVDYISTRARQHKALLLQEIPAISSYRGGGTYTKGAFQQAQIL					
	190	200	210	220	230	240
gi 401	LHARENSTKVFLITDGYSSNGGDPRIAASLRDSGVEIFTFGIWQGNIRELNDMASTPKE					
	190	200	210	220	230	240
SEQ	LHARENSTKVFLITDGYSSNGGDPRIAASLRDSGVEIFTFGIWQGNIRELNDMASTPKE					
	250	260	270	280	290	300
gi 401	EHCYLLHSFEEFEALARRALHEDLPSGSFIQDDMVHCSYLCDEGKDCCDRMGSKCGTHT					
	250	260	270	280	290	300
SEQ	EHCYLLHSFEEFEALARRALHEDLPSGSFIQDDMVHCSYLCDEGKDCCDRMGSKCGTHT					

		310	320	330	340	350	360
gi	401	GHFECICEKGYYGKGLQYECTACPSGTYKPEGSPGGISSCIPCPDENHTSPPGSTSPEDC					
		::					
SEQ		GHFECICEKGYYGKGLQYECTACPSGTYKPEGSPGGISSCIPCPDENHTSPPGSTSPEDC					
		310	320	330	340	350	360
		370	380	390	400	410	420
gi	401	VCREGYRASGQTCELVHCPALKPPENGYFIQNTCNNHFNAACGVRCHPGFDLVGSSIILC					
		::					
SEQ		VCREGYRASGQTCELVHCPALKPPENGYFIQNTCNNHFNAACGVRCHPGFDLVGSSIILC					
		370	380	390	400	410	420
		430	440	450	460	470	480
gi	401	LPNGLWSGSESYCRVRTCPHLRQPKHGHISCSTREMLYKTTCLVACDEGYRLEGSDKLTC					
		::					
SEQ		LPNGLWSGSESYCRVRTCPHLRQPKHGHISCSTREMLYKTTCLVACDEGYRLEGSDKLTC					
		430	440	450	460	470	480
		490	500	510	520	530	540
gi	401	QGNSQWDGPEPRCVERHCSTFQMPKDIIISPHNCGKQPAKFGTICYVSCRQGFILSGVKE					
		::					
SEQ		QGNSQWDGPEPRCVERHCSTFQMPKDVIISPHNCGKQPAKFGTICYVSCRQGFILSGVKE					
		490	500	510	520	530	540
		550	560	570	580	590	600
gi	401	MLRCTTSGKWNVGVQAAVCKDVEAPQINCPKDIEAKTLEQQDSANVTWQIPTAKDNSGEK					
		::					
SEQ		MLRCTTSGKWNVGVQAAVCKDVEAPQINCPKDIEAKTLEQQDSANVTWQIPTAKDNSGEK					
		550	560	570	580	590	600
		610	620	630	640	650	660
gi	401	VSVHVHPAFTPPYLFPPVGDAIVYTATDLSGNQASCIFHIKVIDAEPPVIDWCRSPPPVQ					
		::					
SEQ		VSVHVHPAFTPPYLFPIGDVAIVYTATDLSGNQASCIFHIKVIDAEPPVIDWCRSPPPVQ					
		610	620	630	640	650	660
		670	680	690	700	710	720
gi	401	VSEKVHAASWDEPQFSDNSGAELVITRSHTQGDLPQGETIVQYTATDPSGNNRTCDIHI					
		::					
SEQ		VSEKVHAASWDEPQFSDNSGAELVITRSHTQGDLPQGETIVQYTATDPSGNNRTCDIHI					
		670	680	690	700	710	720
		730	740	750	760	770	780
gi	401	VIKGSPCEIPFTPVNGDFICTPDNTGVNCTLTCLGYDFTEGSTDKYYCAYEDGVWKPTY					
		::					
SEQ		VIKGSPCEIPFTPVNGDFICTPDNTGVNCTLTCLGYDFTEGSTDKYYCAYEDGVWKPTY					
		730	740	750	760	770	780
		790	800	810	820	830	840
gi	401	TTEWPDCAKKRFANHGFKSFEMFYKAARCDTDLMKKFSEAFETTLGKMVPSFCSDAEDI					
		::					
SEQ		TTEWPDCAKKRFANHGFKSFEMFYKAARCDTDLMKKFSEAFETTLGKMVPSFCSDAEDI					
		790	800	810	820	830	840

		850	860	870	880	890	900
gi	401	DCRLEENLTKKYCLEYNYDYENGFAIGPGGWGAANRLDYSYDDFLDTVQETATSIGNAKS					
		::					
SEQ		DCRLEENLTKKYCLEYNYDYENGFAIGPGGWGAANRLDYSYDDFLDTVQETATSIGNAKS					
		850	860	870	880	890	900
		910	920	930	940	950	960
gi	401	SRIKRSAPLSDYKIKLIFNITASVPLPDERNDTLEWENQQRLLQTLETITNKLKRTLND					
		::					
SEQ		SRIKRSAPLSDYKIKLIFNITASVPLPDERNDTLEWENQQRLLQTLETITNKLKRTLND					
		910	920	930	940	950	960
		970	980	990	1000	1010	1020
gi	401	PMYSFQLASEILIADSNLSLETKKASPFRCRPGSVLRGRMCVNCPLGTYYNLEHFTCESCRI					
		::					
SEQ		PMYSFQLASEILIADSNLSLETKKASPFRCRPGSVLRGRMCVNCPLGTYYNLEHFTCESCRI					
		970	980	990	1000	1010	1020
		1030	1040	1050	1060	1070	1080
gi	401	GSYQDEEGQLECKLCPSGMYTEYIHSRNISDCKAQCKQGTYSYSGLETCECPLGTYPK					
		::					
SEQ		GSYQDEEGQLECKLCPSGMYTEYIHSRNISDCKAQCKQGTYSYSGLETCECPLGTYPK					
		1030	1040	1050	1060	1070	1080
		1090	1100	1110	1120	1130	1140
gi	401	FGSRSLSCPENTSTVKGAVNISACGVPCPEGKFSRSGLMPCHPCPRDYYQPNAGKAF					
		::					
SEQ		FGSRSLSCPENTSTVKGAVNISACGVPCPEGKFSRSGLMPCHPCPRDYYQPNAGKAF					
		1090	1100	1110	1120	1130	1140
		1150	1160	1170	1180	1190	1200
gi	401	LACPFYGTTPFAGRSITECSSFSSTFSAAEESVPPASLGHIKKRHEISSQVFHECFN					
		::					
SEQ		LACPFYGTTPFAGRSITECSSFSSTFSAAEESVPPASLGHIKKRHEISSQVFHECFN					
		1150	1160	1170	1180	1190	1200
		1210	1220	1230	1240	1250	1260
gi	401	PCHNSGTCQQLGRGYVCLCPLGYTGLKCETDIDECSPCLNNGVCKDLVGEFICECP					
		PSG					
		::					
SEQ		PCHNSGTCQQLGRGYVCLCPLGYTGLKCETDIDECSPCLNNGVCKDLVGEFICECP					
		1210	1220	1230	1240	1250	1260
		1270	1280	1290	1300	1310	1320
gi	401	YTQRCEENINECSSSPCLNKGICVDGVAGYRCTCVKGFVGLHCETEVNECQSNPCLNNA					
		::					
SEQ		YTQRCEENINECSSSPCLNKGICVDGVAGYRCTCVKGFVGLHCETEVNECQSNPCLNNA					
		1270	1280	1290	1300	1310	1320
		1330	1340	1350	1360	1370	1380
gi	401	VCEDQVGGFLCKCPPGFLGTRCGKNVDECLSQPCKNGATCKDGANSFRCLCAAGFTGSHC					
		::					
SEQ		VCEDQVGGFLCKCPPGFLGTRCGKNVDECLSQPCKNGATCKDGANSFRCLCAAGFTGSHC					
		1330	1340	1350	1360	1370	1380

		1390	1400	1410	1420	1430	1440
gi 401	ELNINECQSNPCRNQATCVDELNSYSCKCQPGFSGKRCETE	QSTGFNLD	FEVSGIYGYVM				
	.....						
SEQ	ELNINECQSNPCRNQATCVDELNSYSCKCQPGFSGQRCETE	QSTGFNLD	FEVSGIYGYVM				
		1390	1400	1410	1420	1430	1440
		1450	1460	1470	1480	1490	1500
gi 401	LDGMLPSLHALTCTFWMKSSDDMNYGTPISYAVDNGSDNTLLL	TDYNGWVLYVNGREKIT					
	.....						
SEQ	LDGMLPSLHALTCTFWMKSSDDMNYGTPISYAVDNGSDNTLLL	TDYNGWVLYVNGREKIT					
		1450	1460	1470	1480	1490	1500
		1510	1520	1530	1540	1550	1560
gi 401	NCPSVNDGRWHHIAITWTSANGIWKVYIDGKLS	DGGAGLSVGLPIPGGGALVLGQE	QDKK				
	.....						
SEQ	NCPSVNDGRWHHIAITWTSANGIWKVYIDGKLS	DGGAGLSVGLPIPGGGALVLGQE	QDKK				
		1510	1520	1530	1540	1550	1560
		1570	1580	1590	1600	1610	1620
gi 401	GEGFSPAESFVGSISQLNLWDYVLS	PQQVKS	LATSCPEELSKGNVLAWP	DFLSGIVGKVK			
	.....						
SEQ	GEGFSPAESFVGSISQLNLWDYVLS	PQQVKS	LATSCPEELSKGNVLAWP	DFLSGIVGKVK			
		1570	1580	1590	1600	1610	1620
		1630	1640	1650	1660	1670	1680
gi 401	IDSKSIFCSDCPRLGGSVPHLRTASE	DLKPGSKVNLFCDPGFQ	LVGNPVQYCLNQ	GQWTQ			
	.....						
SEQ	IDSKSIFCSDCPRLGGSVPHLRTASE	DLKPGSKVNLFCDPGFQ	LVGNPVQYCLNQ	GQWTQ			
		1630	1640	1650	1660	1670	1680
		1690	1700	1710	1720	1730	1740
gi 401	PLPHCERISCGVPPPLENGFHSAD	FYAGSTVTYQC	NNGYLLGDSRMFCTD	NGSWNGVS			
	.....						
SEQ	PLPHCERISCGVPPPLENGFHSAD	FYAGSTVTYQC	NNGYLLGDSRMFCTD	NGSWNGVS			
		1690	1700	1710	1720	1730	1740
		1750	1760	1770	1780	1790	1800
gi 401	PSCLDVDECAVSDCSEHASCLNVDG	SYICSCVPPYTGDGKNCAEPIKCKAPGN	PENGHS				
	.....						
SEQ	PSCLDVDECAVSDCSEHASCLNVDG	SYICSCVPPYTGDGKNCAEPIKCKAPGN	PENGHS				
		1750	1760	1770	1780	1790	1800
		1810	1820	1830	1840	1850	1860
gi 401	SGEIYTVGA	EVTFS	CQEGYQLMGVTKITCLES	GEWNHLIPYCKAVSCGKPAIPENG	CIEE		
	.....						
SEQ	SGEIYTVGA	AAVTF	SQEGYQLMGVTKITCLES	GEWNHLIPYCKAVSCGKPAIPENG	CIEE		
		1810	1820	1830	1840	1850	1860
		1870	1880	1890	1900	1910	1920
gi 401	LAFTFGSKVTYRCNKGYTL	AGDKESSCLANSSWSHSP	PPVCEPVKCSSPENINNGKYILSG				
	.....						
SEQ	LAFTFGSKVTYRCNKGYTL	AGDKESSCLANSSWSHSP	PPVCEPVKCSSPENINNGKYILSG				
		1870	1880	1890	1900	1910	1920

		1930	1940	1950	1960	1970	1980
gi 401	LTYLSTASYSCDTGYSLQGPSII	ECTASGIWDRAPPACHLVFCGEPPAIKDAVITGNNFT					
SEQ	LTYLSTASYSCDTGYSLQGPSII	ECTASGIWDRAPPACHLVFCGEPPAIKDAVITGNNFT					
		1930	1940	1950	1960	1970	1980
		1990	2000	2010	2020	2030	2040
gi 401	FRNTVITYTCKEGYTLAGLDTIE	CLADGKWSRSDQQCLAVSCDEPPIVDHASPETAHRLFG					
SEQ	FRNTVITYTCKEGYTLAGLDTIE	CLADGKWSRSDQQCLAVSCDEPPIVDHASPETAHRLFG					
		1990	2000	2010	2020	2030	2040
		2050	2060	2070	2080	2090	2100
gi 401	DIAFYCYSDGYSLADNSQLLCNA	QKGWVPPEGQDMPRCIAHFCEKPPSVSYSILESVSKA					
SEQ	DIAFYCYSDGYSLADNSQLLCNA	QKGWVPPEGQDMPRCIAHFCEKPPSVSYSILESVSKA					
		2050	2060	2070	2080	2090	2100
		2110	2120	2130	2140	2150	2160
gi 401	KFAAGSVVSFKCMEGFVLNTSAK	IECMRGGQWNPSPMSIQICIPVRCGEPPSIMNGYASGS					
SEQ	KFAAGSVVSFKCMEGFVLNTSAK	IECMRGGQWNPSPMSIQICIPVRCGEPPSIMNGYASGS					
		2110	2120	2130	2140	2150	2160
		2170	2180	2190	2200	2210	2220
gi 401	NYSFGAMVAYSCNKGFIYKGEKK	STCEATGQWSSPIPTCHPVSCGEPPKVENGFLHTTG					
SEQ	NYSFGAMVAYSCNKGFIYKGEKK	STCEATGQWSSPIPTCHPVSCGEPPKVENGFLHTTG					
		2170	2180	2190	2200	2210	2220
		2230	2240	2250	2260	2270	2280
gi 401	RIFESEVRYQCNPYGKSVGSPV	FVCQANRHHWSESPLMCVPLDCGKPPPIQNGFMKGENT					
SEQ	RIFESEVRYQCNPYGKSVGSPV	FVCQANRHHWSESPLMCVPLDCGKPPPIQNGFMKGENT					
		2230	2240	2250	2260	2270	2280
		2290	2300	2310	2320	2330	2340
gi 401	EVGSKVQFFCNEGYELVGDSSW	TCQKSGKWNKSNPKCMPAKCEPPLLENQLVLKELTT					
SEQ	EVGSKVQFFCNEGYELVGDSSW	TCQKSGKWNKSNPKCMPAKCEPPLLENQLVLKELTT					
		2290	2300	2310	2320	2330	2340
		2350	2360	2370	2380	2390	2400
gi 401	EVGVVTFSCKEGHVLQGPSVLK	CLPSQQWNSFPVCKIVLCTPPPLISFGVPIPSALHF					
SEQ	EVGVVTFSCKEGHVLQGPSVLK	CLPSQQWNSFPVCKIVLCTPPPLISFGVPIPSALHF					
		2350	2360	2370	2380	2390	2400
		2410	2420	2430	2440	2450	2460
gi 401	GSTVKYSCVGGFFLRGNSTTLC	QPDGTWSSPLPECVPVECPQPEEIPNGIIDVQGLAYLS					
SEQ	GSTVKYSCVGGFFLRGNSTTLC	QPDGTWSSPLPECVPVECPQPEEIPNGIIDVQGLAYLS					
		2410	2420	2430	2440	2450	2460

		2470	2480	2490	2500	2510	2520
gi 401	TALYTCKPGFELVGNTTTL	CGENGHWLGGKPTCKAIECLKPKEILNGKFSYTD	DLHYGQTV				
SEQ	TALYTCKPGFELVGNTTTL	CGENGHWLGGKPTCKAIECLKPKEILNGKFSYTD	DLHYGQTV				
		2470	2480	2490	2500	2510	2520
		2530	2540	2550	2560	2570	2580
gi 401	TYSCNRGFRLEGPSALT	CLETGDWDVDAPSCNAIHCDSPQPIENG	FVEGADYSYGAI	IIY			
SEQ	TYSCNRGFRLEGPSALT	CLETGDWDVDAPSCNAIHCDSPQPIENG	FVEGADYSYGAI	IIY			
		2530	2540	2550	2560	2570	2580
		2590	2600	2610	2620	2630	2640
gi 401	SCFPGFQVAGHAMQT	CEESGWSSSIPTCMPIDCGLPPHIDFGDCT	KLKDDQGYFEQ	EDDM			
SEQ	SCFPGFQVAGHAMQT	CEESGWSSSIPTCMPIDCGLPPHIDFGDCT	KLKDDQGYFEQ	EDDM			
		2590	2600	2610	2620	2630	2640
		2650	2660	2670	2680	2690	2700
gi 401	MEVPYVTPHPPYHL	GAVAKTWENTKESPATHSSN	FLYGTMVSYTCNPGYELLGN	PVLI	CQ		
SEQ	MEVPYVTPHPPYHL	GAVAKTWENTKESPATHSSN	FLYGTMVSYTCNPGYELLGN	PVLI	CQ		
		2650	2660	2670	2680	2690	2700
		2710	2720	2730	2740	2750	2760
gi 401	EDGTWNGSAPSCISIE	CDLPTAPENGFLRFTETSMGSAVQYSCKPGHIL	VGSDLRLCLEN				
SEQ	EDGTWNGSAPSCISIE	CDLPTAPENGFLRFTETSMGSAVQYSCKPGHIL	AGSDLRLCLEN				
		2710	2720	2730	2740	2750	2760
		2770	2780	2790	2800	2810	2820
gi 401	RKWSGASPRCEAIS	CKKPNPVMNGSIKGSNYTYLSTLYYECD	PGYVLNGTERRTCQDDKN				
SEQ	RKWSGASPRCEAIS	CKKPNPVMNGSIKGSNYTYLSTLYYECD	PGYVLNGTERRTCQDDKN				
		2770	2780	2790	2800	2810	2820
		2830	2840	2850	2860	2870	2880
gi 401	WDEDEPICIPVDCSS	PPVSANGQVRGDEYTFQKEIEYTCNEGFLLEGARS	RVCLANGSWS				
SEQ	WDEDEPICIPVDCSS	PPVSANGQVRGDEYTFQKEIEYTCNEGFLLEGARS	RVCLANGSWS				
		2830	2840	2850	2860	2870	2880
		2890	2900	2910	2920	2930	2940
gi 401	GATPDCVPVRCATPP	QLANGVTEGLDYGF	MKEVTFHCHEGYILHGAPKL	TCQSDGNWDAE			
SEQ	GATPDCVPVRCATPP	QLANGVTEGLDYGF	MKEVTFHCHEGYILHGAPKL	TCQSDGNWDAE			
		2890	2900	2910	2920	2930	2940
		2950	2960	2970	2980	2990	3000
gi 401	IPLCKPVNCGPPED	LAHGFPNGFSFIHGGHIQYQCFPGYKLHGNSSRRCL	SNGSWSGSSP				
SEQ	IPLCKPVNCGPPED	LAHGFPNGFSFIHGGHIQYQCFPGYKLHGNSSRRCL	SNGSWSGSSP				
		2950	2960	2970	2980	2990	3000

		3010	3020	3030	3040	3050	3060
gi 401	SCLPCRSTP	VIEYGT	VNGTDF	DCGKAARI	QCFKGF	KLLGLSEIT	CEADGQWSSGFPHCE
	.....						
SEQ	SCLPCRSTP	VIEYGT	VNGTDF	DCGKAARI	QCFKGF	KLLGLSEIT	CEADGQWSSGFPHCE
		3010	3020	3030	3040	3050	3060
		3070	3080	3090	3100	3110	3120
gi 401	HTSCGSLPMIPNAFIS	ETSSWKEN	VITYSCRS	GYVIQGS	SDLICTE	KGVWSQ	PYPVCEPL
	.....						
SEQ	HTSCGSLPMIPNAFIS	ETSSWKEN	VITYSCRS	GYVIQGS	SDLICTE	KGVWSQ	PYPVCEPL
		3070	3080	3090	3100	3110	3120
		3130	3140	3150	3160	3170	3180
gi 401	SCGSPPSVANAVATGE	AHTYESE	VKLRCLE	GYTMDT	DTDTFT	CQKDGR	WPPERISCSPKK
	.....						
SEQ	SCGSPPSVANAVATGE	AHTYESE	VKLRCLE	GYTMDT	DTDTFT	CQKDGR	WPPERISCSPKK
		3130	3140	3150	3160	3170	3180
		3190	3200	3210	3220	3230	3240
gi 401	CPLPENITHILVHGDD	FSVNRQ	VS	SVSCAEG	YTFEGV	NISVCQ	LDGTWEPPFSDESCSPVS
	.....						
SEQ	CPLPENITHILVHGDD	FSVNRQ	VS	SVSCAEG	YTFEGV	NISVCQ	LDGTWEPPFSDESCSPVS
		3190	3200	3210	3220	3230	3240
		3250	3260	3270	3280	3290	3300
gi 401	CGKPESPEHGFVVG	SKYT	FESTII	YQCEP	GYELEG	NRERV	CQENRQWSGGVAICKETRCE
	.....						
SEQ	CGKPESPEHGFVVG	SKYT	FESTII	YQCEP	GYELEG	NRERV	CQENRQWSGGVAICKETRCE
		3250	3260	3270	3280	3290	3300
		3310	3320	3330	3340	3350	3360
gi 401	TPLEFLNGKADIENRT	TGPNVV	YSCNRG	YSLEGP	SEAHCT	TENGTW	SHPVPLCKPNPCPVP
	.....						
SEQ	TPLEFLNGKADIENRT	TGPNVV	YSCNRG	YSLEGP	SEAHCT	TENGTW	SHPVPLCKPNPCPVP
		3310	3320	3330	3340	3350	3360
		3370	3380	3390	3400	3410	3420
gi 401	FVIPENALLSEKEFY	VDQNV	SIKCRE	GFL	LQGHGI	ITCNP	DETWTQTSACEKISCGPPA
	.....						
SEQ	FVIPENALLSEKEFY	VDQNV	SIKCRE	GFL	LQGHGI	ITCNP	DETWTQTSACEKISCGPPA
		3370	3380	3390	3400	3410	3420
		3430	3440	3450	3460	3470	3480
gi 401	HVENAIARGVHYQY	GDMITY	SCYSGM	LEGFL	RSVCL	ENGTW	TSPPICRAVCRFPCQNGG
	.....						
SEQ	HVENAIARGVHYQY	GDMITY	SCYSGM	LEGFL	RSVCL	ENGTW	TSPPICRAVCRFPCQNGG
		3430	3440	3450	3460	3470	3480
		3490	3500	3510	3520	3530	3540
gi 401	ICQRPNACSCPEGW	MGR	LCEEP	I	CILPCL	NGGRC	VAPYQDCPPGWTGSRCHTAVCQSPC
	.....						
SEQ	ICQRPNACSCPEGW	MGR	LCEEP	I	CILPCL	NGGRC	VAPYQDCPPGWTGSRCHTAVCQSPC
		3490	3500	3510	3520	3530	3540

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          3550      3560      3570
gi|401 LNKGKCVRPNRCHCLSSWTGHNCSRKRRTGF
      :
SEQ    LNKGKCVRPNRCHCLSSWTGHNCSRKRRTGF
          3550      3560      3570
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3571 residues in 1 query sequences

3571 residues in 1 library sequences

Scomplib [version 3.3t05 March 30, 2000]

start: Wed Mar 3 12:05:29 2004 done: Wed Mar 3 12:05:40 2004

Scan time: 0.117 Display time: 18.567

Function used was FASTA